

SEQUENCE LISTING

<110> Nomura , Hitoshi
Maeda, Masatsugu

<120> NOVEL HEMOPOIETIN RECEPTOR PROTEINS

<130> 12660-002001

<140> US 09/720,285

<141> 2000-12-21

<150> PCT/JP99/03351

<151> 1999-06-23

<150> JP 10/297409

<151> 1998-10-19

<150> JP 10/214720

<151> 1998-06-24

<160> 213

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 361

<212> PRT

<213> Homo sapiens

<400> 1

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Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly
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Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
20          25          30
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
35          40          45
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
50          55          60
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
65          70          75          80
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
85          90          95
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
100         105         110
Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
115         120         125
Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
130         135         140
Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
145         150         155         160
Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
165         170         175
Ser Val Asp Ser Arg Ser Val Ser Leu Pro Leu Glu Phe Arg Lys
180         185         190
Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser

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<210> 2
<211> 1934
<212> DNA
<213> Homo sapiens
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<400> 2							
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gcgtctggcc	ctctgcctgc	ctctccctga	gtgtggctga	cagccacgca	gctgtgtctg		120
tctgtctgcg	gcccgatcat	ccctgctgcg	gccgcctggt	accttccttg	ccgtctcttt		180
cctctgtctg	ctgctctgtg	ggacacctgc	ctggaggccc	agctgcccg	catcagagtg		240
acaggtctta	tgacagcctg	attggtgact	cgggctgggt	gtggattctc	acccaggcc		300
tctgctgct	ttctcagacc	ctcatctgtc	acccccacgc	tgaaccagc	tgccaccccc		360
agaagcccat	cagactgccc	ccagcacacg	gaatggattt	ctgagaaaga	agccgaaaca		420
gaaggcccg	gggagtcagc	atg ccg cgt	ggc tgg gcc	gcc ccc ttg	ctc ctg		473
		Met Pro Arg	Gly Trp Ala	Ala Pro Leu	Leu Leu		
		1	5	10			

gat tac ctc cag acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac 569
Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His
30 35 40

ccc agc acg ctc acc ctt acc tgg caa gac cag tat gaa gag ctg aag 617
Pro Ser Thr Leu Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys
45 50 55

gac gag gcc acc tcc tgc agc ctc cac agg tgc gcc cac aat gcc acg 665
Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr

60	65	70	75	
cat gcc acc tac acc tgc cac atg gat gta ttc cac ttc atg gcc gac His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe Met Ala Asp	80	85	90	713
gac att ttc agt gtc aac atc aca gac cag tct ggc aac tac tcc cag Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln	95	100	105	761
gag tgt ggc agc ttt ctc ctg gct gag agc atc aag ccg gct ccc cct Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro	110	115	120	809
ttc aac gtg act gtg acc ttc tca gga cag tat aat atc tcc tgg cgc Phe Asn Val Thr Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg	125	130	135	857
tca gat tac gaa gac cct gcc ttc tac atg ctg aag ggc aag ctt cag Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln	140	145	150	905
tat gag ctg cag tac agg aac cgg gga gac ccc tgg gct gtg agt ccg Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro	160	165	170	953
agg aga aag ctg atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro	175	180	185	1001
ctg gag ttc cgc aaa gac tcg agc tat gag ctg cag gtg cgg gca ggg Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly	190	195	200	1049
ccc atg cct ggc tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp	205	210	215	1097
ccg gtc atc ttt cag acc cag tca gag gag tta aag gaa ggc tgg aac Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn	220	225	230	1145
cct cac ctg ctg ctt ctc ctc ctg ctt gtc ata gtc ttc att cct gcc Pro His Leu Leu Leu Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala	240	245	250	1193
ttc tgg agc ctg aag acc cat cca ttg tgg agg cta tgg aag aag ata Phe Trp Ser Leu Lys Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile	255	260	265	1241
tgg gcc gtc ccc agc cct gag cgg ttc ttc atg ccc ctg tac aag ggc Trp Ala Val Pro Ser Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly	270	275	280	1289
tgc agc gga gac ttc aag aaa tgg gtg ggt gca ccc ttc act ggc tcc Cys Ser Gly Asp Phe Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser	285	290	295	1337

agc ctg gag ctg gga ccc tgg agc cca gag gtg ccc tcc acc ctg gag 1385
 Ser Leu Glu Leu Gly Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu
 300 305 310 315

gtg tac agc tgc cac cca ccc agc agc cct gtg gag tgt gac ttc acc 1433
 Val Tyr Ser Cys His Pro Pro Ser Ser Pro Val Glu Cys Asp Phe Thr
 320 325 330

agc ccc ggg gac gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg 1481
 Ser Pro Gly Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val
 335 340 345

gtc att cct ccg cca ctt tcg agc cct gga ccc cag gcc agc 1523
 Val Ile Pro Pro Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
 350 355 360

taatgaggct gactggatgt ccagagctgg ccaggccact gggccctgag ccagagacaa 1583
 gggtcacctgg gctgtgatgt gaagacacct gcagcctttg gtctcctgga tgggcctttg 1643
 agcctgatgt ttacagtgtc tgtgtgtgtg tgcataatgtg tgtgtgtgca tatgcatgtg 1703
 tgtgtgtgtg tgtgtcttag gtgcgcagtg gcatgtccac gtgtgtgtga ttgcacgtgc 1763
 ctgtgggcct gggataatgc ccatggtact ccatgcattc acctgccctg tgcattgtctg 1823
 gactcacgga gctcacccat gtgcacaagt gtgcacagta aacgtgtttg tgggtcaacag 1883
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1934

<210> 3
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 3
 Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly
 1 5 10 15
 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
 20 25 30
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 35 40 45
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 50 55 60
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 65 70 75 80
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 85 90 95
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Leu Leu Ala Glu Ser Lys Ser Glu Glu Lys Ala Asp Leu Ser Gly Leu
 115 120 125
 Lys Lys Cys Leu Pro Pro Pro Pro Gly Val Pro Gln Arg Leu Glu Leu
 130 135 140

<210> 4
 <211> 1779
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (441)...(872)

<400> 4

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ggcagccagc ggcctcagac agaccactg gcgtctctct gctgagtgc cgtaagctcg      60
gcgtctggcc ctctgcctgc ctctccctga gtgtggctga cagccacgca gctgtgtctg     120
tctgtctgcg gcccgtgcat ccctgctgcg gccgcctggg accttccttg ccgtctcttt     180
cctctgtctg ctgctctgtg ggacacctgc ctggaggccc agctgcccggt catcagagtgc    240
acaggtctta tgacagcctg attggtgact cgggctgggt gtggattctc accccaggcc      300
tctgcctgct ttctcagacc ctcatctgtc acccccacgc tgaaccacgc tgccaccccc     360
agaagcccat cagactgccc ccagcacacg gaatggattt ctgagaaaga agccgaaaca      420
gaaggcccggt gggagtcagc atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg      473

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Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu

1

5

10

```

ctg ctg ctc cag gga ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc      521
Leu Leu Leu Gln Gly Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr
                15                      20                      25

```

```

gat tac ctc cag acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac      569
Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His
                30                      35                      40

```

```

ccc agc acg ctc acc ctt acc tgg caa gac cag tat gaa gag ctg aag      617
Pro Ser Thr Leu Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys
                45                      50                      55

```

```

gac gag gcc acc tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg      665
Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr
                60                      65                      70                      75

```

```

cat gcc acc tac acc tgc cac atg gat gta ttc cac ttc atg gcc gac      713
His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe Met Ala Asp
                80                      85                      90

```

```

gac att ttc agt gtc aac atc aca gac cag tct ggc aac tac tcc cag      761
Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln
                95                      100                      105

```

```

gag tgt ggc agc ttt ctc ctg gct gag agc aag tcc gag gag aaa gct      809
Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Lys Ser Glu Glu Lys Ala
                110                      115                      120

```

```

gat ctc agt gga ctc aag aag tgt ctc cct cct ccc cct gga gtt ccg      857
Asp Leu Ser Gly Leu Lys Lys Cys Leu Pro Pro Pro Pro Gly Val Pro
                125                      130                      135

```

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caa aga ctc gag cta tgagctgcag gtgcgggcag ggcccatgcc tggctcctcc      912
Gln Arg Leu Glu Leu
140

```

```

taccagggga cctggagtga atggagtgc cgggtcatct ttcagaccca gtcagaggag      972
ttaaaggaag gctggaaccc tcacctgctg cttctcctcc tgcttgctcat agtcttcatt    1032
cctgccttct ggagcctgaa gacctatcca ttgtggaggc tatggaagaa gatatgggcc      1092
gtccccagcc ctgagcgggt cttcatgccc ctgtacaagg gctgcagcgg agacttcaag      1152
aaatgggtgg gtgcaccctt cactggctcc agcctggagc tgggaccctg gagcccagag      1212
gtgccctcca ccctggaggt gtacagctgc caccaccca gcagccctgt ggagtgtgac      1272
ttcaccagcc ccggggacga aggaccccc cggagctacc tccgccagtg ggtggtcatt      1332

```

```

cctccgccac tttcgagccc tggaccccag gccagctaata gaggctgact ggatgtccag 1392
agctggccag gccactgggc cctgagccag agacaaggctc acctgggctg tgatgtgaag 1452
acacctgcag cctttggtct cctggatggg cctttgagcc tgatgtttac agtgtctgtg 1512
tgtgtgtgca tatgtgtgtg tgtgcatatg catgtgtgtg tgtgtgtgtg tcttaggtgc 1572
gcagtggcat gtccacgtgt gtgtgattgc acgtgcctgt gggcctggga taatgcccac 1632
ggtactccat gcattcacct gccctgtgca tgtctggact cacggagctc acccatgtgc 1692
acaagtgtgc acagtaaacg tgtttgtggt caacagaaaa aaaaaaaaaa aaaaaaaaaa 1752
aaaaaaaaaa aaaaaaaaaa aaaaaaa 1779

```

```

<210> 5
<211> 237
<212> PRT
<213> Homo sapiens

```

```

<400> 5
Met Pro Arg Met Pro Pro Thr Pro Ala Thr Trp Met Tyr Ser Thr Ser
1          5          10          15
Trp Pro Thr Thr Phe Ser Val Ser Thr Ser Gln Thr Ser Leu Ala Thr
          20          25          30
Thr Pro Arg Ser Val Ala Ala Phe Ser Trp Leu Arg Ala Ser Pro Arg
          35          40          45
Arg Lys Leu Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu
          50          55          60
Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro
65          70          75          80
Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro
          85          90          95
Val Ile Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro
          100          105          110
His Leu Leu Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe
          115          120          125
Trp Ser Leu Lys Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp
          130          135          140
Ala Val Pro Ser Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys
145          150          155          160
Ser Gly Asp Phe Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser
          165          170          175
Leu Glu Leu Gly Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val
          180          185          190
Tyr Ser Cys His Pro Pro Ser Ser Pro Val Glu Cys Asp Phe Thr Ser
          195          200          205
Pro Gly Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val
          210          215          220
Ile Pro Pro Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
225          230          235

```

```

<210> 6
<211> 1779
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (658)...(1368)

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<400> 6
ggcagccagc ggccctcagac agaccactg gcgtctctct gctgagtgac cgtaagctcg 60

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 tctgtctgcg gcccgtgcat ccctgctgcg gccgctggt accttccttg ccgtctcttt 180
 cctctgtctg ctgctctgtg ggacacctgc ctggaggccc agctgcccgt catcagagt 240
 acaggtctta tgacagcctg attggtgact cgggctgggt gtggattctc accccaggcc 300
 tctgectgct ttctcagacc ctcatctgtc acccccacgc tgaaccacgc tgccaccccc 360
 agaagcccat cagactgccc ccagcacacg gaatggattt ctgagaaaga agccgaaaca 420
 gaaggcccgt gggagtcagc atgccgcgtg gctggggccgc ccccttgctc ctgctgctgc 480
 tccagggagg ctggggctgc cccgacctcg tctgctacac cgattacctc cagacgggtca 540
 tctgcatcct ggaaatgtgg aacctccacc ccagcacgct cacccttacc tggcaagacc 600
 agtatgaaga gctgaaggac gaggccaect cctgcagcct ccacaggctg gccaca atg 660
 Met
 1

cca cgc atg cca cct aca cct gcc aca tgg atg tat tcc act tca tgg 708
 Pro Arg Met Pro Pro Thr Pro Ala Thr Trp Met Tyr Ser Thr Ser Trp
 5 10 15

ccg acg aca ttt tca gtg tca aca tca cag acc agt ctg gca act act 756
 Pro Thr Thr Phe Ser Val Ser Thr Ser Gln Thr Ser Leu Ala Thr Thr
 20 25 30

ccc agg agt gtg gca gct ttc tcc tgg ctg aga gca agt ccg agg aga 804
 Pro Arg Ser Val Ala Ala Phe Ser Trp Leu Arg Ala Ser Pro Arg Arg
 35 40 45

aag ctg atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag 852
 Lys Leu Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu
 50 55 60 65

ttc cgc aaa gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg 900
 Phe Arg Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met
 70 75 80

cct ggc tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc 948
 Pro Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val
 85 90 95

atc ttt cag acc cag tca gag gag tta aag gaa ggc tgg aac cct cac 996
 Ile Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His
 100 105 110

ctg ctg ctt ctc ctc ctg ctt gtc ata gtc ttc att cct gcc ttc tgg 1044
 Leu Leu Leu Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp
 115 120 125

agc ctg aag acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc 1092
 Ser Leu Lys Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala
 130 135 140 145

gtc ccc agc cct gag cgg ttc ttc atg ccc ctg tac aag ggc tgc agc 1140
 Val Pro Ser Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser
 150 155 160

gga gac ttc aag aaa tgg gtg ggt gca ccc ttc act ggc tcc agc ctg 1188
 Gly Asp Phe Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu
 165 170 175

```

gag ctg gga ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac      1236
Glu Leu Gly Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr
      180              185              190

agc tgc cac cca ccc agc agc cct gtg gag tgt gac ttc acc agc ccc      1284
Ser Cys His Pro Pro Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro
      195              200              205

ggg gac gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att      1332
Gly Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile
      210              215              220              225

cct ccg cca ctt tcg agc cct gga ccc cag gcc agc taatgaggct          1378
Pro Pro Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
      230              235

gactggatgt ccagagctgg ccaggccact gggccctgag ccagagacaa ggtcacctgg      1438
gctgtgatgt gaagacacct gcagcctttg gtctcctgga tgggcctttg agcctgatgt      1498
ttacagtgtc tgtgtgtgtg tgcataatgtg tgtgtgtgca tatgcatgtg tgtgtgtgtg      1558
tgtgtccttag gtgcgcagtg gcatgtccac gtgtgtgtga ttgcacgtgc ctgtgggcct      1618
gggataatgc ccatggtact ccatgcattc acctgccttg tgcattgtctg gactcacgga      1678
gctcacccat gtgcacaagt gtgcacagta aacgtgtttg tggtaacag aaaaaaaaaa      1738
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a
                                             1779

```

<210> 7
 <211> 538
 <212> PRT
 <213> Homo sapiens

```

<400> 7
Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly
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Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
      20      25      30
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
      35      40      45
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
      50      55      60
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
      65      70      75      80
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
      85      90      95
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
      100      105      110
Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
      115      120      125
Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
      130      135      140
Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
      145      150      155      160
Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
      165      170      175
Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
      180      185      190
Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
      195      200      205
Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln

```


210		215		220
Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu				
225		230		235
Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys				240
	245		250	255
Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser				
	260		265	270
Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe				
	275		280	285
Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly				
	290		295	300
Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His				
305		310		315
Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu				320
	325		330	335
Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp				
	340		345	350
Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp				
	355		360	365
Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala				
	370		375	380
Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro				
385		390		395
Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp				400
	405		410	415
Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser				
	420		425	430
Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg				
	435		440	445
Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro				
	450		455	460
Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser				
465		470		475
Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly				480
	485		490	495
Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp				
	500		505	510
Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro				
	515		520	525
Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser				
530		535		

<210> 8

<211> 2465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (441)...(2054)

<400> 8

ggcagccagc	ggcctcagac	agaccactg	gcgtctctct	gctgagtgac	cgtaagctcg	60
gcgtctggcc	ctctgcctgc	ctctccctga	gtgtggctga	cagccacgca	gctgtgtctg	120
tctgtctgcg	ccccgtgcat	ccctgctgcg	gccgcctggg	accttccttg	ccgtctcttt	180
cctctgtctg	ctgctctgtg	ggacacctgc	ctggaggccc	agctgcccg	catcagagtg	240
acaggcttta	tgacagcctg	attggtgact	cgggctgggt	gtggattctc	accccaggcc	300

tctgcttgc	ttctcagacc	ctcatctgtc	acccccacgc	tgaaccacgc	tgccaccccc	360
agaagcccat	cagactgccc	ccagcacacg	gaatggattt	ctgagaaaga	agccgaaaca	420
gaaggcccg	gggagtcagc	atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg	Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu	473		
		1	5	10		
ctg ctg ctc cag gga ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc	521					
Leu Leu Leu Gln Gly Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr						
15	20	25				
gat tac ctc cag acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac	569					
Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His						
30	35	40				
ccc agc acg ctc acc ctt acc tgg caa gac cag tat gaa gag ctg aag	617					
Pro Ser Thr Leu Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys						
45	50	55				
gac gag gcc acc tcc tgc agc ctc cac agg tgc gcc cac aat gcc acg	665					
Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr						
60	65	70	75			
cat gcc acc tac acc tgc cac atg gat gta ttc cac ttc atg gcc gac	713					
His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe Met Ala Asp						
80	85	90				
gac att ttc agt gtc aac atc aca gac cag tct ggc aac tac tcc cag	761					
Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln						
95	100	105				
gag tgt ggc agc ttt ctc ctg gct gag agc atc aag ccg gct ccc cct	809					
Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro						
110	115	120				
ttc aac gtg act gtg acc ttc tca gga cag tat aat atc tcc tgg cgc	857					
Phe Asn Val Thr Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg						
125	130	135				
tca gat tac gaa gac cct gcc ttc tac atg ctg aag ggc aag ctt cag	905					
Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln						
140	145	150	155			
tat gag ctg cag tac agg aac cgg gga gac ccc tgg gct gtg agt ccg	953					
Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro						
160	165	170				
agg aga aag ctg atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc	1001					
Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro						
175	180	185				
ctg gag ttc cgc aaa gac tgc agc tat gag ctg cag gtg cgg gca ggg	1049					
Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly						
190	195	200				
ccc atg cct ggc tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac	1097					
Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp						
205	210	215				

ccg gtc atc ttt cag acc cag tca gag gag tta aag gaa ggc tgg aac	1145
Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn	
220 225 230 235	
cct cac ctg ctg ctt ctc ctc ctg ctt gtc ata gtc ttc att cct gcc	1193
Pro His Leu Leu Leu Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala	
240 245 250	
ttc tgg agc ctg aag acc cat cca ttg tgg agg cta tgg aag aag ata	1241
Phe Trp Ser Leu Lys Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile	
255 260 265	
tgg gcc gtc ccc agc cct gag cgg ttc ttc atg ccc ctg tac aag ggc	1289
Trp Ala Val Pro Ser Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly	
270 275 280	
tgc agc gga gac ttc aag aaa tgg gtg ggt gca ccc ttc act ggc tcc	1337
Cys Ser Gly Asp Phe Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser	
285 290 295	
agc ctg gag ctg gga ccc tgg agc cca gag gtg ccc tcc acc ctg gag	1385
Ser Leu Glu Leu Gly Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu	
300 305 310 315	
gtg tac agc tgc cac cca cca cgg agc ccg gcc aag agg ctg cag ctc	1433
Val Tyr Ser Cys His Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu	
320 325 330	
acg gag cta caa gaa cca gca gag ctg gtg gag tct gac ggt gtg ccc	1481
Thr Glu Leu Gln Glu Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro	
335 340 345	
aag ccc agc ttc tgg ccg aca gcc cag aac tcg ggg ggc tca gct tac	1529
Lys Pro Ser Phe Trp Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr	
350 355 360	
agt gag gag agg gat cgg cca tac ggc ctg gtg tcc att gac aca gtg	1577
Ser Glu Glu Arg Asp Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val	
365 370 375	
act gtg cta gat gca gag ggg cca tgc acc tgg ccc tgc agc tgt gag	1625
Thr Val Leu Asp Ala Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu	
380 385 390 395	
gat gac ggc tac cca gcc ctg gac ctg gat gct ggc ctg gag ccc agc	1673
Asp Asp Gly Tyr Pro Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser	
400 405 410	
cca ggc cta gag gac cca ctc ttg gat gca ggg acc aca gtc ctg tcc	1721
Pro Gly Leu Glu Asp Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser	
415 420 425	
tgt ggc tgt gtc tca gct ggc agc cct ggg cta gga ggg ccc ctg gga	1769
Cys Gly Cys Val Ser Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly	
430 435 440	

agc ctc ctg gac aga cta aag cca ccc ctt gca gat ggg gag gac tgg 1817
 Ser Leu Leu Asp Arg Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp
 445 450 455

gct ggg gga ctg ccc tgg ggt ggc cgg tca cct gga ggg gtc tca gag 1865
 Ala Gly Gly Leu Pro Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu
 460 465 470 475

agt gag gcg ggc tca ccc ctg gcc ggc ctg gat atg gac acg ttt gac 1913
 Ser Glu Ala Gly Ser Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp
 480 485 490

agt ggc ttt gtg ggc tct gac tgc agc agc cct gtg gag tgt gac ttc 1961
 Ser Gly Phe Val Gly Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe
 495 500 505

acc agc ccc ggg gac gaa gga ccc ccc cgg agc tac ctc cgc cag tgg 2009
 Thr Ser Pro Gly Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp
 510 515 520

gtg gtc att cct ccg cca ctt tcg agc cct gga ccc cag gcc agc 2054
 Val Val Ile Pro Pro Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
 525 530 535

taatgaggct gactggatgt ccagagctgg ccaggccact gggccctgag ccagagacaa 2114
 ggtcacctgg gctgtgatgt gaagacacct gcagcctttg gtctcctgga tgggcctttg 2174
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 gactcacgga gctcacccat gtgcacaagt gtgcacagta aacgtgtttg tgggtcaacag 2414
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2465

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

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ccggctcccc ctttcaacgt gactgtgacc

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<210> 10

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<213> Artificial Sequence

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ggcaagcttc agtatgagct gcagtacagg

30

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

<400> 11

accctctgac tgggtctgaa agatgaccgg

30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

<400> 12

catgggcctt gcccgcacct gcagtcata

30

<210> 13

<211> 1128

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1125)

<400> 13

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Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly
1 5 10 15

48

ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg
Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
20 25 30

96

gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
35 40 45

144

ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
50 55 60

192

tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
65 70 75 80

240

tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
85 90 95

288

aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
100 105 110

336

ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val 115 120 125	384
acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp 130 135 140	432
cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr 145 150 155 160	480
agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile 165 170 175	528
tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys 180 185 190	576
gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser 195 200 205	624
tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln 210 215 220	672
acc cag tca gag acc gcc tgg atc tcc ttg gtg acc gct ctg cat cta Thr Gln Ser Glu Thr Ala Trp Ile Ser Leu Val Thr Ala Leu His Leu 225 230 235 240	720
gtg ctg ggc ctc agc gcc gtc ctg ggc ctg ctg ctg ctg agg tgg cag Val Leu Gly Leu Ser Ala Val Leu Gly Leu Leu Leu Leu Arg Trp Gln 245 250 255	768
ttt cct gca cac tac agg aga ctg agg cat gcc ctg tgg ccc tca ctt Phe Pro Ala His Tyr Arg Arg Leu Arg His Ala Leu Trp Pro Ser Leu 260 265 270	816
cca gac ctg cac cgg gtc cta ggc cag tac ctt agg gac act gca gcc Pro Asp Leu His Arg Val Leu Gly Gln Tyr Leu Arg Asp Thr Ala Ala 275 280 285	864
ctg agc ccg ccc aag gcc aca gtc tca gat acc tgt gaa gaa gtg gaa Leu Ser Pro Pro Lys Ala Thr Val Ser Asp Thr Cys Glu Glu Val Glu 290 295 300	912
ccc agc ctc ctt gaa atc ctc ccc aag tcc tca gag agg act cct ttg Pro Ser Leu Leu Glu Ile Leu Pro Lys Ser Ser Glu Arg Thr Pro Leu 305 310 315 320	960
ccc ctg tgt tcc tcc cag gcc cag atg gac tac cga aga ttg cag cct Pro Leu Cys Ser Ser Gln Ala Gln Met Asp Tyr Arg Arg Leu Gln Pro 325 330 335	1008
tct tgc ctg ggg acc atg ccc ctg tct gtg tgc cca ccc atg gct gag	1056

Ser Cys Leu Gly Thr Met Pro Leu Ser Val Cys Pro Pro Met Ala Glu
 340 345 350

tca ggg tcc tgc tgt acc acc cac att gcc aac cat tcc tac cta cca 1104
 Ser Gly Ser Cys Cys Thr Thr His Ile Ala Asn His Ser Tyr Leu Pro
 355 360 365

cta agc tat tgg cag cag cct tga 1128
 Leu Ser Tyr Trp Gln Gln Pro
 370 375

<210> 14
 <211> 375
 <212> PRT
 <213> Homo sapiens

<400> 14
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 1 5 10 15
 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
 20 25 30
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 35 40 45
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 50 55 60
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 65 70 75 80
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 85 90 95
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 115 120 125
 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 130 135 140
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 180 185 190
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ser Glu Thr Ala Trp Ile Ser Leu Val Thr Ala Leu His Leu
 225 230 235 240
 Val Leu Gly Leu Ser Ala Val Leu Gly Leu Leu Leu Leu Arg Trp Gln
 245 250 255
 Phe Pro Ala His Tyr Arg Arg Leu Arg His Ala Leu Trp Pro Ser Leu
 260 265 270
 Pro Asp Leu His Arg Val Leu Gly Gln Tyr Leu Arg Asp Thr Ala Ala
 275 280 285
 Leu Ser Pro Pro Lys Ala Thr Val Ser Asp Thr Cys Glu Glu Val Glu
 290 295 300
 Pro Ser Leu Leu Glu Ile Leu Pro Lys Ser Ser Glu Arg Thr Pro Leu
 305 310 315 320

Pro	Leu	Cys	Ser	Ser	Gln	Ala	Gln	Met	Asp	Tyr	Arg	Arg	Leu	Gln	Pro
				325					330					335	
Ser	Cys	Leu	Gly	Thr	Met	Pro	Leu	Ser	Val	Cys	Pro	Pro	Met	Ala	Glu
			340					345					350		
Ser	Gly	Ser	Cys	Cys	Thr	Thr	His	Ile	Ala	Asn	His	Ser	Tyr	Leu	Pro
		355					360					365			
Leu	Ser	Tyr	Trp	Gln	Gln	Pro									
	370					375									

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<210> 15
<211> 1383
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1) ... (1380)
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<400>	15															
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Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly																
1 5 10 15																
ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg	96															
Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr																
20 25 30																
gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc	144															
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr																
35 40 45																
ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc	192															
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser																
50 55 60																
tgc agc ctc cac agg tgc gcc cac aat gcc acg cat gcc acc tac acc	240															
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr																
65 70 75 80																
tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc	288															
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val																
85 90 95																
aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt	336															
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe																
100 105 110																
ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg	384															
Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val																
115 120 125																
acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac	432															
Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp																
130 135 140																
cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac	480															
Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr																

145	150	155	160	
agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc				528
Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile	165	170	175	
tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa				576
Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys	180	185	190	
gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc				624
Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser	195	200	205	
tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag				672
Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln	210	215	220	
acc cag tca gag gag ccc aaa tct tgt gac aaa act cac aca tgc cca				720
Thr Gln Ser Glu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	225	230	235	240
ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc				768
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe	245	250	255	
ccc cca aaa ccc aag gac acc ctc atg atc tcc ccg acc cct gag gtc				816
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	260	265	270	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc				864
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	275	280	285	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg				912
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	290	295	300	
cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc				960
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	305	310	315	320
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc				1008
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	325	330	335	
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc				1056
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	340	345	350	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg				1104
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	355	360	365	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc				1152
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	370	375	380	

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg 1200
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 385 390 395 400

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc 1248
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 405 410 415

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 1296
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 420 425 430

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 1344
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 435 440 445

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1383
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455 460

<210> 16

<211> 460

<212> PRT

<213> Homo sapiens

<400> 16

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 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
 20 25 30
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 35 40 45
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 50 55 60
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 65 70 75 80
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 85 90 95
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 115 120 125
 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 130 135 140
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 180 185 190
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ser Glu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 225 230 235 240

Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
245								250				255				
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
260								265				270				
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
275								280				285				
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
290								295				300				
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
305					310				315				320			
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
				325				330				335				
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
340								345				350				
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
355								360				365				
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
370								375				380				
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
385					390				395				400			
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	
				405				410				415				
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	
420								425				430				
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	
435								440				445				
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
450								455				460				

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<210> 17
<211> 477
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) ... (474)
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<400> 17																	
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Met	Pro	Arg	Gly	Trp	Ala	Ala	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Gly		
1				5					10					15			
ggc	tgg	ggc	tgc	ccc	gac	ctc	gtc	tgc	tac	acc	gat	tac	ctc	cag	acg	96	
Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr		
			20					25					30				
gtc	atc	tgc	atc	ctg	gaa	atg	tgg	aac	ctc	cac	ccc	agc	acg	ctc	acc	144	
Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr		
		35					40					45					
ctt	acc	tgg	caa	gac	cag	tat	gaa	gag	ctg	aag	gac	gag	gcc	acc	tcc	192	
Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser		
	50					55					60						
tgc	agc	ctc	cac	agg	tgc	gcc	cac	aat	gcc	acg	cat	gcc	acc	tac	acc	240	
Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr		

65	70	75	80	
tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc				288
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val				
	85	90	95	
aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt				336
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe				
	100	105	110	
ctc ctg gct gag agc aag tcc gag gag aaa gct gat ctc agt gga ctc				384
Leu Leu Ala Glu Ser Lys Ser Glu Glu Lys Ala Asp Leu Ser Gly Leu				
	115	120	125	
aag aag tgt ctc cct cct ccc cct gga gtt ccg caa aga ctc gag cta				432
Lys Lys Cys Leu Pro Pro Pro Pro Gly Val Pro Gln Arg Leu Glu Leu				
	130	135	140	
agg gcg cgc cag gac tac aag gac gac gat gac aag acg cgt				474
Arg Ala Arg Gln Asp Tyr Lys Asp Asp Asp Asp Lys Thr Arg				
	145	150	155	
taa				477

<210> 18
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 18
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Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
20 25 30
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
35 40 45
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
50 55 60
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
65 70 75 80
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
85 90 95
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
100 105 110
Leu Leu Ala Glu Ser Lys Ser Glu Glu Lys Ala Asp Leu Ser Gly Leu
115 120 125
Lys Lys Cys Leu Pro Pro Pro Pro Gly Val Pro Gln Arg Leu Glu Leu
130 135 140
Arg Ala Arg Gln Asp Tyr Lys Asp Asp Asp Asp Lys Thr Arg
145 150 155

<210> 19
 <211> 144
 <212> PRT
 <213> Mus musculus

<400> 19

Met	Pro	Arg	Gly	Trp	Ala	Ala	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Gly
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Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr
		20						25					30		
Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr
		35					40					45			
Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser
		50				55					60				
Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr
65					70					75				80	
Ser	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val
			85						90					95	
Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Phe	Gln	Glu	Cys	Gly	Ser	Phe
			100					105					110		
Leu	Arg	Ala	Glu	Ser	Lys	Ser	Glu	Lys	Ala	Asp	Leu	Ser	Gly	Leu	
		115					120				125				
Lys	Lys	Cys	Leu	Pro	Pro	Pro	Pro	Gly	Val	Pro	Gln	Arg	Leu	Glu	Leu
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<210> 20

<211> 1960

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (439)...(870)

<400> 20

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tgtctgcggc	ccgtgcatcc	ctgctgcggc	cgcttggtac	cttccttgcc	gtctctttcc	180
tctgtctgct	gctctgtggg	acacctgcct	ggaggcccag	ctgcccgtca	tcagagtgc	240
aggtcttatg	acagcctgat	tggtgactcg	ggctgggtgt	ggattctcac	cccaggcctc	300
tgctgctttt	ctcagaccct	catcggtcac	ccccacgctg	aaccagctg	ccaccccag	360
aagcccatca	gactgcccc	agcacacgga	atggatttct	gagaaagaag	ccgaaacaga	420
aggcccgtgg	gagtcagc	atg ccg cgt ggc tgg gcc	gcc tcc ttg ctc ctg			471
	Met	Pro	Arg	Gly	Trp	Ala
	1			5		10
ctg ctg ctc	cag gga ggc	tgg ggc tgc	ccc gac ctc	gtc tgc tac	acc	519
Leu Leu Leu	Gln Gly Gly	Trp Gly Cys	Pro Asp Leu	Val Cys Tyr	Thr	
	15		20		25	
gat tac ctc	cag acg gtc	atc tgc atc	ctg gaa atg	tgg aac ctc	cac	567
Asp Tyr Leu	Gln Thr Val	Ile Cys Ile	Leu Glu Met	Trp Asn Leu	His	
	30		35		40	
ccc agc acg	ctc acc ctt	acc tgg caa	gac cag tat	gaa gag ctg	aag	615
Pro Ser Thr	Leu Thr Leu	Thr Trp Gln	Asp Gln Tyr	Glu Glu Leu	Lys	
	45		50		55	
gac gag gcc	acc tcc tgc	agc ctc cac	agg tcg gcc	cac aat gcc	acg	663
Asp Glu Ala	Thr Ser Cys	Ser Leu His	Arg Ser Ala	His Asn Ala	Thr	
	60		65		70	
cat gcc acc	tac acc agc	cac atg gat	gta ttc cac	ttc atg gcc	gac	711

His Ala Thr Tyr Thr Ser His Met Asp Val Phe His Phe Met Ala Asp
80 85 90

gac att ttc agt gtc aac atc aca gac cag tct ggc aac tac ttc cag 759
Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Phe Gln
95 100 105

gag tgt ggc agc ttt ctc cgg gct gag agc aag tcc gag gag aaa gct 807
Glu Cys Gly Ser Phe Leu Arg Ala Glu Ser Lys Ser Glu Glu Lys Ala
110 115 120

gat ctc agt gga ctc aag aag tgt ctc cct cct ccc cct gga gtt ccg 855
Asp Leu Ser Gly Leu Lys Lys Cys Leu Pro Pro Pro Pro Gly Val Pro
125 130 135

caa aga ctc gag cta tgagctgcag gtgcgggcag ggcccatgcc tggctcctcc 910
Gln Arg Leu Glu Leu
140

taccagggga cctggagtga atggagtgc cgggtcatct ttcagaccca gtcagaggag 970
ttaaaggaag gctggaaccc tcacctgctg cttctcctcc tgcttgctcat agtcttcatt 1030
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<210> 21

<211> 538

<212> PRT

<213> Mus musculus

<400> 21

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Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
20 25 30

Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
35 40 45

Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
50 55 60

Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
65 70 75 80

Ser His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
85 90 95

Asn Ile Thr Asp Gln Ser Gly Asn Tyr Phe Gln Glu Cys Gly Ser Phe

			100					105				110			
Leu	Arg	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val
		115					120					125			
Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Arg	Arg	Ser	Asp	Tyr	Glu	Asp
	130					135					140				
Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr
145					150					155				160	
Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile
			165						170				175		
Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys
		180						185				190			
Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser
	195						200				205				
Ser	Tyr	Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln
	210					215				220					
Thr	Gln	Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Leu	Leu	Leu
225					230					235				240	
Leu	Leu	Leu	Leu	Val	Ile	Val	Phe	Ile	Pro	Ala	Phe	Trp	Ser	Leu	Lys
			245						250				255		
Thr	His	Pro	Leu	Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Val	Pro	Ser
	260							265				270			
Pro	Glu	Arg	Phe	Phe	Met	Pro	Leu	Tyr	Lys	Gly	Cys	Ser	Gly	Asp	Phe
	275					280				285					
Lys	Lys	Trp	Val	Gly	Ala	Pro	Phe	Thr	Gly	Ser	Ser	Leu	Glu	Leu	Gly
	290					295				300					
Pro	Trp	Ser	Pro	Glu	Val	Pro	Ser	Thr	Leu	Glu	Val	Tyr	Ser	Cys	His
305					310					315				320	
Pro	Pro	Arg	Ser	Pro	Ala	Lys	Arg	Leu	Gln	Leu	Thr	Glu	Leu	Gln	Glu
			325						330				335		
Pro	Ala	Glu	Leu	Val	Glu	Ser	Asp	Gly	Val	Pro	Lys	Pro	Ser	Phe	Trp
	340							345				350			
Pro	Thr	Ala	Gln	Asn	Ser	Gly	Gly	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp
	355					360					365				
Arg	Pro	Tyr	Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	Thr	Val	Leu	Asp	Ala
	370					375					380				
Glu	Gly	Pro	Cys	Thr	Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro
385					390					395				400	
Ala	Leu	Asp	Leu	Asp	Ala	Gly	Leu	Glu	Pro	Ser	Pro	Gly	Leu	Glu	Asp
			405						410				415		
Pro	Leu	Leu	Asp	Ala	Gly	Thr	Thr	Val	Leu	Ser	Cys	Gly	Cys	Val	Ser
		420						425				430			
Ala	Gly	Ser	Pro	Gly	Leu	Gly	Gly	Pro	Leu	Gly	Ser	Leu	Leu	Asp	Arg
	435					440					445				
Leu	Lys	Pro	Pro	Leu	Ala	Asp	Gly	Glu	Asp	Trp	Ala	Gly	Gly	Leu	Pro
	450					455					460				
Trp	Gly	Gly	Arg	Ser	Pro	Gly	Gly	Val	Ser	Glu	Ser	Glu	Ala	Gly	Ser
465					470					475				480	
Pro	Leu	Ala	Gly	Leu	Asp	Met	Asp	Thr	Phe	Asp	Ser	Gly	Phe	Val	Cys
			485						490				495		
Ser	Asp	Cys	Ser	Ser	Pro	Val	Glu	Cys	Asp	Phe	Thr	Ser	Pro	Gly	Asp
	500							505				510			
Glu	Gly	Pro	Pro	Arg	Ser	Tyr	Leu	Arg	Gln	Trp	Val	Val	Ile	Pro	Pro
	515						520					525			
Pro	Leu	Ser	Ser	Pro	Gly	Pro	Gln	Ala	Ser						
	530					535									

<211> 2115
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (439)...(2052)

<400> 22
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 tgtctgcggc ccgtgcatcc ctgctgcggc cgccctggtag ctcccttgcc gtctctttcc 180
 tctgtctgct gctctgtggg acacctgcct ggaggcccag ctgcccgtca tcagagtgc 240
 aggtcttatg acagcctgat tggtagctcg ggctgggtgt ggattctcac cccaggcctc 300
 tgccctgcttt ctcagaccct catcggtcac cccacgctg aaccagctg ccaccccag 360
 aagcccatca gactgcccc agcacacgga atggatttct gagaaagaag ccgaaacaga 420
 agggccgtgg gagtgcagc atg ccg cgt ggc tgg gcc gcc tcc ttg ctc ctg 471
 Met Pro Arg Gly Trp Ala Ala Ser Leu Leu Leu
 1 5 10
 ctg ctg ctc cag gga ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc 519
 Leu Leu Leu Gln Gly Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr
 15 20 25
 gat tac ctc cag acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac 567
 Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His
 30 35 40
 ccc agc acg ctc acc ctt acc tgg caa gac cag tat gaa gag ctg aag 615
 Pro Ser Thr Leu Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys
 45 50 55
 gac gag gcc acc tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg 663
 Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr
 60 65 70 75
 cat gcc acc tac acc agc cac atg gat gta ttc cac ttc atg gcc gac 711
 His Ala Thr Tyr Thr Ser His Met Asp Val Phe His Phe Met Ala Asp
 80 85 90
 gac att ttc agt gtc aac atc aca gac cag tct ggc aac tac ttc cag 759
 Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Phe Gln
 95 100 105
 gag tgt ggc agc ttt ctc cgg gct gag agc atc aag ccg gct ccc cct 807
 Glu Cys Gly Ser Phe Leu Arg Ala Glu Ser Ile Lys Pro Ala Pro Pro
 110 115 120
 ttc aac gtg act gtg acc ttc tca gga cag tat aat atc tcc agg cgc 855
 Phe Asn Val Thr Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Arg Arg
 125 130 135
 tca gat tac gaa gac cct gcc ttc tac atg ctg aag ggc aag ctt cag 903
 Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln
 140 145 150 155
 tat gag ctg cag tac agg aac cgg gga gac ccc tgg gct gtg agt ccg 951

Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	
				160					165					170		
agg	aga	aag	ctg	atc	tca	gtg	gac	tca	aga	agt	gtc	tcc	ctc	ctc	ccc	999
Arg	Arg	Lys	Leu	Ile	Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	
			175					180				185				
ctg	gag	ttc	cgc	aaa	gac	tcg	agc	tat	gag	ctg	cag	gtg	cgg	gca	ggg	1047
Leu	Glu	Phe	Arg	Lys	Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	
		190					195				200					
ccc	atg	cct	ggc	tcc	tcc	tac	cag	ggg	acc	tgg	agt	gaa	tgg	agt	gac	1095
Pro	Met	Pro	Gly	Ser	Ser	Tyr	Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	
	205					210				215						
ccg	gtc	atc	ttt	cag	acc	cag	tca	gag	gag	tta	aag	gaa	ggc	tgg	aac	1143
Pro	Val	Ile	Phe	Gln	Thr	Gln	Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	
220				225				230							235	
cct	cac	ctg	ctg	ctt	ctc	ctc	ctg	ctt	gtc	ata	gtc	ttc	att	cct	gcc	1191
Pro	His	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Val	Ile	Val	Phe	Ile	Pro	Ala	
				240				245					250			
ttc	tgg	agc	ctg	aag	acc	cat	cca	ttg	tgg	agg	cta	tgg	aag	aag	ata	1239
Phe	Trp	Ser	Leu	Lys	Thr	His	Pro	Leu	Trp	Arg	Leu	Trp	Lys	Lys	Ile	
			255				260					265				
tgg	gcc	gtc	ccc	agc	cct	gag	cgg	ttc	ttc	atg	ccc	ctg	tac	aag	ggc	1287
Trp	Ala	Val	Pro	Ser	Pro	Glu	Arg	Phe	Phe	Met	Pro	Leu	Tyr	Lys	Gly	
	270					275					280					
tgc	agc	gga	gac	ttc	aag	aaa	tgg	gtg	ggc	gca	ccc	ttc	act	ggc	tcc	1335
Cys	Ser	Gly	Asp	Phe	Lys	Lys	Trp	Val	Gly	Ala	Pro	Phe	Thr	Gly	Ser	
	285				290					295						
agc	ctg	gag	ctg	gga	ccc	tgg	agc	cca	gag	gtg	ccc	tcc	acc	ctg	gag	1383
Ser	Leu	Glu	Leu	Gly	Pro	Trp	Ser	Pro	Glu	Val	Pro	Ser	Thr	Leu	Glu	
300				305				310						315		
gtg	tac	agc	tgc	cac	cca	cca	cgg	agc	ccg	gcc	aag	agg	ctg	cag	ctc	1431
Val	Tyr	Ser	Cys	His	Pro	Pro	Arg	Ser	Pro	Ala	Lys	Arg	Leu	Gln	Leu	
				320				325					330			
acg	gag	cta	caa	gaa	cca	gca	gag	ctg	gtg	gag	tct	gac	ggc	gtg	ccc	1479
Thr	Glu	Leu	Gln	Glu	Pro	Ala	Glu	Leu	Val	Glu	Ser	Asp	Gly	Val	Pro	
			335				340					345				
aag	ccc	agc	ttc	tgg	ccg	aca	gcc	cag	aac	tcg	ggg	ggc	tca	gct	tac	1527
Lys	Pro	Ser	Phe	Trp	Pro	Thr	Ala	Gln	Asn	Ser	Gly	Gly	Ser	Ala	Tyr	
	350					355					360					
agt	gag	gag	agg	gat	cgg	cca	tac	ggc	ctg	gtg	tcc	att	gac	aca	gtg	1575
Ser	Glu	Glu	Arg	Asp	Arg	Pro	Tyr	Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	
	365				370			375								
act	gtg	cta	gat	gca	gag	ggg	cca	tgc	acc	tgg	ccc	tgc	agc	tgt	gag	1623
Thr	Val	Leu	Asp	Ala	Glu	Gly	Pro	Cys	Thr	Trp	Pro	Cys	Ser	Cys	Glu	

380	385	390	395	
gat gac ggc tac cca gcc ctg gac ctg gat gct ggc ctg gag ccc agc				1671
Asp Asp Gly Tyr Pro Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser				
	400	405	410	
cca ggc cta gag gac cca ctc ttg gat gca ggg acc aca gtc ctg tcc				1719
Pro Gly Leu Glu Asp Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser				
	415	420	425	
tgt ggc tgt gtc tca gct ggc agc cct ggg cta gga ggg ccc ctg gga				1767
Cys Gly Cys Val Ser Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly				
	430	435	440	
agc ctc ctg gac aga cta aag cca ccc ctt gca gat ggg gag gac tgg				1815
Ser Leu Leu Asp Arg Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp				
	445	450	455	
gct ggg gga ctg ccc tgg ggt ggc cgg tca cct gga ggg gtc tca gag				1863
Ala Gly Gly Leu Pro Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu				
	460	465	470	475
agt gag gcg ggc tca ccc ctg gcc ggc ctg gat atg gac acg ttt gac				1911
Ser Glu Ala Gly Ser Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp				
	480	485	490	
agt ggc ttt gtg tgc tct gac tgc agc agc cct gtg gag tgt gac ttc				1959
Ser Gly Phe Val Cys Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe				
	495	500	505	
acc agc ccc ggg gac gaa gga ccc ccc cgg agc tac ctc cgc cag tgg				2007
Thr Ser Pro Gly Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp				
	510	515	520	
gtg gtc att cct ccg cca ctt tcg agc cct gga ccc cag gcc agc				2052
Val Val Ile Pro Pro Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser				
	525	530	535	
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aaa				2115
<210> 23				
<211> 411				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> 3'UTR				
<222> (1) ... (411)				
<400> 23				
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ggtcacctgg gctgtgatgt gaagacacct gcagcctttg gtctcctgga tgggcctttg				120
agcctgatgt ttacagtgtc tgtgtgtgtg tgcataatgtg tgtgtgtgca tatgcatgtg				180
tgtgtgtgtg tgtgtcttag gtgcgcagtg gcatgtccac gtgtgtgtga ttgcacgtgc				240
ctgtgggcct gggataatgc ccatgggtact ccatgcattc acctgccctg tgcatgtctg				300
gactcacgga gctcacccat gtgcacaagt gtgcacagta aacgtgtttg tggccaacag				360

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411

<210> 24
 <211> 877
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 3'UTR
 <222> (1)... (877)

<400> 24

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<220>
 <221> 3'UTR
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<211> 907

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)...(907)

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<210> 27

<211> 3818
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<220>
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 <222> (1) ... (3818)

<400> 27

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<210> 28

<211> 330

<212> DNA

<213> Mus musculus

<400> 28

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<210> 29

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<212> DNA

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<220>

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<210> 31

<211> 15

<212> DNA

<213> Artificial Sequence

<220>
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 <222> 7-9
 <223> n = a, t, c, or g

<400> 31
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<210> 32
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 <213> Artificial Sequence

<220>
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<210> 33
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<220>
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<400> 33
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<210> 34
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<400> 34
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<210> 35
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<400> 35

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<400> 41
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<210> 42
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<400> 42
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<210> 43
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<400> 43
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<400> 45
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<210> 46
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<210> 47
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<220>
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<400> 47
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<210> 48
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<400> 48
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<210> 49
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<400> 49
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<210> 50
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<400> 50
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<210> 51
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<210> 58

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<210> 59

<211> 15

<212> DNA

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<223> Synthetically generated oligonucleotide

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<210> 60

<211> 15

<212> DNA

<213> Artificial Sequence

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<223> Synthetically generated oligonucleotide

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<210> 61

<211> 15

<212> DNA

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 Val Arg Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser Asp Trp Ser
 20 25 30
 Thr Pro Arg Val Phe Thr Thr Gln
 35 40

<210> 195
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 195
 Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro Leu Gln Gly Glu
 1 5 10 15
 Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala Phe Arg Thr Lys
 20 25 30

<210> 196
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 196

Thr	Leu	Leu	Gln	Arg	Lys	Leu	Gln	Pro	Ala	Ala	Met	Tyr	Glu	Ile	Lys
1				5					10					15	
Val	Arg	Ser	Ile	Pro	Asp	His	Tyr	Phe	Lys	Gly	Phe	Trp	Ser	Glu	Trp
			20					25					30		
Ser	Pro	Ser	Tyr	Tyr	Phe	Arg	Thr	Pro	Glu	Ile	Asn	Asn	Ser	Ser	Gly
		35					40					45			
Glu	Met	Asp	Pro	Ile	Leu	Leu									
	50					55									

<210> 197

<211> 43

<212> PRT

<213> Homo sapiens

<400> 197

Thr	Leu	Gly	Pro	Glu	His	Leu	Met	Pro	Ser	Ser	Thr	Tyr	Val	Ala	Arg
1				5					10					15	
Val	Arg	Thr	Arg	Leu	Ala	Pro	Gly	Ser	Arg	Leu	Ser	Gly	Arg	Pro	Ser
			20				25						30		
Lys	Trp	Ser	Pro	Glu	Val	Cys	Trp	Asp	Ser	Gln					
		35					40								

<210> 198

<211> 20

<212> PRT

<213> Homo sapiens

<400> 198

Thr	Gly	Tyr	Asn	Gly	Ile	Trp	Ser	Glu	Trp	Ser	Glu	Ala	Arg	Ser	Trp
1			5						10					15	
Asp	Thr	Glu	Ser												
			20												

<210> 199

<211> 43

<212> PRT

<213> Mus musculus

<400> 199

Asn	Leu	Glu	Pro	Lys	Leu	Phe	Leu	Pro	Asn	Ser	Ile	Tyr	Ala	Ala	Arg
1				5					10					15	
Val	Arg	Thr	Arg	Leu	Ser	Ala	Gly	Ser	Ser	Leu	Ser	Gly	Arg	Pro	Ser
			20				25						30		
Arg	Trp	Ser	Pro	Glu	Val	His	Trp	Asp	Ser	Gln					
		35					40								

<210> 200

<211> 35

<212> PRT

<213> Mus musculus

<400> 200

Gln	Leu	Glu	Pro	Asp	Thr	Ser	Tyr	Cys	Ala	Arg	Val	Arg	Val	Lys	Pro
1				5					10					15	
Ile	Ser	Asp	Tyr	Asp	Gly	Ile	Trp	Ser	Glu	Trp	Ser	Asn	Glu	Tyr	Thr
			20				25						30		

Trp Thr Thr
35

<210> 201
<211> 28
<212> PRT
<213> Homo sapiens

<400> 201
Ser Lys Tyr Asp Val Gln Val Arg Ala Ala Val Ser Ser Met Cys Arg
1 5 10 15
Glu Ala Gly Leu Trp Ser Glu Trp Ser Gln Pro Ile
20 25

<210> 202
<211> 15
<212> PRT
<213> Homo sapiens

<400> 202
Tyr Thr Gly Gln Trp Ser Glu Trp Ser Gln Pro Val Cys Phe Gln
1 5 10 15

<210> 203
<211> 37
<212> PRT
<213> Homo sapiens

<400> 203
Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met Ala Glu
1 5 10 15
Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val Ser Leu
20 25 30
Leu Thr Pro Ser Asp
35

<210> 204
<211> 36
<212> PRT
<213> Homo sapiens

<400> 204
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
1 5 10 15
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
20 25 30
Ser His Pro Ile
35

<210> 205
<211> 33
<212> PRT
<213> Homo sapiens

<400> 205
Leu Cys Pro Leu Glu Met Asn Val Ala Gln Glu Phe Gln Leu Arg Arg
1 5 10 15

Arg Gln Leu Gly Ser Gln Gly Ser Ser Trp Ser Lys Trp Ser Ser Pro
 20 25 30
 Val

<210> 206
 <211> 38
 <212> PRT
 <213> Homo sapiens

<400> 206
 Leu Asp Leu Lys Pro Phe Thr Glu Tyr Glu Phe Gln Ile Ser Ser Lys
 1 5 10 15
 Leu His Leu Tyr Lys Gly Ser Trp Ser Asp Trp Ser Glu Ser Leu Arg
 20 25 30
 Ala Gln Thr Pro Glu Glu
 35

<210> 207
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 207
 His Gln Val Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser
 1 5 10 15
 Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe
 20 25 30
 Tyr Met Leu Lys Gly Lys Leu Gln Tyr
 35 40

<210> 208
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 208
 Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val Thr Ala Val Ala Arg
 1 5 10 15
 Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp Pro His Ser Trp Asn
 20 25 30
 Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg Tyr
 35 40

<210> 209
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 209
 Tyr Lys Val Lys Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn Ser
 1 5 10 15
 Glu Glu Leu Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn Pro Ser Ile
 20 25 30
 Lys Ser Val Ile Ile Leu Lys Tyr Asn Ile Gln Tyr
 35 40

<210> 210
 <211> 30
 <212> PRT
 <213> Rattus norvegicus

<400> 210
 Val Lys Pro Asp Pro Pro Leu Gly Leu Arg Met Glu Val Thr Asp Asp
 1 5 10 15
 Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr Lys Ala Pro
 20 25 30

<210> 211
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 211
 Val Pro Ser Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser
 1 5 10 15
 Gly Asp Phe Lys
 20

<210> 212
 <211> 20
 <212> PRT
 <213> Mus musculus

<400> 212
 Ile Pro Ser Pro Glu Ala Phe Phe His Pro Leu Tyr Ser Val Tyr His
 1 5 10 15
 Gly Asp Phe Gln
 20

<210> 213
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 213
 Val Pro Ser Pro Ala Met Phe Phe Gln Pro Leu Tyr Ser Val His Asn
 1 5 10 15
 Gly Asn Phe Gln
 20